

[illegible]

Human genome derived cDNA or cDNA libraries generated for
analyzing gene expression in human cervical epithelial cells -
claim 27: SEQ ID No. 22809; 487bp; final seq.

The present invention relates to human stromal exon nucleic acid probes
(*Sino* - see A110008 A1/2455). The present sequence is a peptide encoded
by the said probe. The SINDs are derived from human beta cells. The SINDs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of the cancer, notably
cervical cancer.

Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WHO
at <http://www.hiv/patb/patb1/shed/pet/sequences>.

AA	SS	Stimulus	F54 AA;				
Uncy Match	88.98;	Score 28.04;	106.22;	Length	F54;		
Post-Local Stimulati	98.58;	PCC; R ₂ 2	50.220;				
Matches	F46;	Conservative	8;	Inputs	4;	Outputs	1

6d	NI	PI	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	123
1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111
011	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	123	62	
05	123	1111	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	183
10d	62	1111	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	129
09	181	1111	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	243
10b	123	1111	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	180
09	243	1111	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	103
10c	181	1111	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	212
001	123	1111	VS	IS	VA	IM	VA	IP	PI	IM	HANS	IG	GM	LD	SQ	QV	OM	VS	IT	SV	VS	FN	VA	164

[illegible][illegible]

RESULTS

AAM0491
II AAM0491 standard; Protein; 564 AA.
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A: AAM0491;
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17 x1 zool (first entry)
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XX
Caption #128 created by probe for measuring placental gene expression.
XX Primary microarray; human; placenta; antenatal diagnosis;
XX genotype disorder;

[illegible]

58 Human genome-derived single exon nucleic acid probes useful for
59 analyzing gene expression in human placenta
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Claim 27, SEQ ID NO 30760, 6544p, English.

The present invention relates to single exon nucleic acid probes (herein
See AA14115-AA15540). The present sequence is a peptide encoded by one
such probe. The probes are useful for predicting a mutation for
predicting, monitoring and displaying gene expression in samples derived
from human placenta. The probes are useful for antenatal diagnosis of
human genetic disorders.

Sequence F44 AA:

[illegible]

ID# 400 T00TNNIRK02AATSA 348

Search completed: September 4, 2002, 09:04:50
Job time: 159 sec

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07 194 CTH-EVLLLELVLPYVEETKVLAEAP AAGHTNLAIVHLLTHVFL 245
   | : | : | : | : | : | : | : | : | : | : | : | : |
08 221 FSHIVATLALVYVYARLALQVAFQCHIAAFAASRAVAVIMLVAF-- 278
   | : | : | : | : | : | : | : | : | : | : | : | : |
09 241 FAVWTPVRLVLA AVEIKKACKFNNLLTAATLAVRSGGLFAVYTHLNR 402
   | : | : | : | : | : | : | : | : | : | : | : | : |
10 279 FPLSNPLKALILLLEGGALVQL NVYVATFLALIAFPGSSGLTTCYTHNR 477
   | : | : | : | : | : | : | : | : | : | : | : | : |
11 293 KRYVTFHMMHRIFFGLISGIRKPLASTLAAFAHAGVAMGLFAAGVAF 492
   | : | : | : | : | : | : | : | : | : | : | : | : |
12 348 KQFOAAF-----RMLC----- 449
   | : | : | : | : | : | : | : | : | : | : | : | : |
13 364 MVRVHTLGLAAVHTPLASGHRFQSSAYFSSASTHGSVSGTAAVTHRP 421
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14 350 -----PPSSSHKAVSRPGMLHRRPVVAFPSDIDISE 486
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15 422 SGRKPSASHRK 433
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16 387 SG---PSSNAPR 395
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RESULT 15

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0924G9 FREELIMINARY PRG: 432 AA.
0924G9:
01 01-083-2001 (FRESHDEL: 19, Created)
01 01-083-2001 (FRESHDEL: 19, Last sequence update)
01 01-083-2001 (FRESHDEL: 19, Last annotation update)
01 NEUROPEPTIDE NPVF RECEPTOR.
08 Rattus norvegicus (Rat).
08 Fukuyama; Metazoa; Chordata; Craniata; Vertebrata; (not custom);
08 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
08 NCBI_LinID 10115.
08 111
08 SEQUENCE FROM N.A.
08 Liu G., Guan X.-M., McDonald T.P., Jiang Q., Zeng Z., Marlene J.,
08 Williams D.L., Jr., Hong Y., Figueroa D., Clements M.K., Malloe J.,
08 Wang R., Evans J., Gould R., Austin C.P.:
08 "Identification and characterization of two cognate receptors for
08 mammalian FMRFamide-like neuropeptides."
08 Submitted (1997-2000) to the EMBL/Genbank/DBJ databases.
08 EMBL: AF330676; AA094200.1;
08 Receptor.
08 SEQUENCE 432 AA; 48171 MW; EAFDF0527967688A CRC64;

```

Query Match

```

10.5% Score 44.5; DB:1; Length 432;
Best local similarity 27.6%; Pctd. NG: 7, 46-17;
Matches 88; Conservative 64; Mismatches 124; Indels 43; Gaps 9;

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09 25 FAFIFPMGAMVITVYVLENSPVLLAVFKKRLKNSGTFVSSVAMVAVITVPL 84
   | : | : | : | : | : | : | : | : | : | : | : | : |
10 41 FVAAMPF-AAVVLILLCTVGNITVYPLVKRRIRIVTRNGTIRLAVSRFVGLRPT 99
   | : | : | : | : | : | : | : | : | : | : | : | : |
11 95 MLEASISQWLSQWQWVPTTQNSVSTFNVAIAINRYVICHSELYETFSVN 144
   | : | : | : | : | : | : | : | : | : | : | : | : |
12 100 TLVINLITGMPEDNATKMSGLVQMSVASVFTLVAIAVERKCIWH PPRKILTRK 157
   | : | : | : | : | : | : | : | : | : | : | : | : |
13 145 IFTVVIIMIVLAVLNNYIGILE-----YDKI---VTCLENNIN--NIVET 189
   | : | : | : | : | : | : | : | : | : | : | : | : |
14 158 ALFTIAVIALALIMPSAVLITVTRIHRETLANKKVTIYECWAWMIRKRSVTT 217
   | : | : | : | : | : | : | : | : | : | : | : | : |
15 190 VITWIVHVELLIVGFFVYVITKVLAAPEA--GNTNGLAVYVNTLRF 249
   | : | : | : | : | : | : | : | : | : | : | : | : |
16 219 AVIPAHIVVPLAVVYVYVLAEPICVAPSHAPGFEAVAFDRTSGKAVYVHMLAV 277
   | : | : | : | : | : | : | : | : | : | : | : | : |
17 241 VITLFAVWKTIVNTVYVAVSRIMAKITFN WYLAATFATNLSNNAV 292
   | : | : | : | : | : | : | : | : | : | : | : | : |
18 278 ALF--FTLSMLTLLILLY-----GLSEHGLHLSVYVPLAHMLAFHSSANPI 329
   | : | : | : | : | : | : | : | : | : | : | : | : |
19 293 IYGLINRPRRYWTFIHA 311
   | : | : | : | : | : | : | : | : | : | : | : | : |

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GenCore version 1.5
Copyright (c) 1993 - 2000 Computer Ltd.

00M protein - protein search, using sw model

Run on: September 4, 2002, 09:01:16, search time 14.15 seconds
(with last all hom 422)
1764.690 Million cell updates/sec

Title: US-09-628-495d-1
Perfect score: 3256
Sequence: 1 MDTTAVTPTGCTGCKLQ.....NNTHTVWVWHPHPRNAV 613

Scoring table:
Gapop 10.0, Gapext 0.5

Searches: 109224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 109224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1 SwissProt_40*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3256	100.0	613	1	MILX_HUMAN
2	2318	71.2	575	1	MILX_SHEEP
3	2234	68.6	583	1	MILX_MOUSE
4	937.5	28.8	345	1	MILX_CHICK
5	904.5	27.8	420	1	MILX_XENLA
6	891.5	27.4	350	1	MILX_HUMAN
7	887.5	27.3	353	1	MILX_MOUSE
8	886.5	27.2	353	1	MILX_MOUSE
9	879.5	27.0	353	1	MILX_MOUSE
10	864.5	26.7	466	1	MILX_SHEEP
11	854.5	26.2	462	1	MILX_HUMAN
12	797	24.5	289	1	MILX_CHICK
13	692	21.3	257	1	MILX_MOUSE
14	591	16.9	119	1	MILX_MOUSE
15	465	14.3	151	1	MILX_MOUSE
16	434	13.3	156	1	MILX_MOUSE
17	424	13.0	154	1	MILX_MOUSE
18	418	12.8	154	1	MILX_MOUSE
19	416	12.8	152	1	MILX_MOUSE
20	411	12.6	157	1	MILX_MOUSE
21	409.5	12.4	152	1	MILX_MOUSE
22	398	12.2	151	1	MILX_MOUSE
23	350.5	10.8	142	1	MILX_MOUSE
24	345.5	10.6	142	1	MILX_MOUSE
25	341	10.5	142	1	MILX_MOUSE
26	339	10.4	143	1	MILX_MOUSE
27	338	10.4	143	1	MILX_MOUSE
28	336	10.3	143	1	MILX_MOUSE
29	332.5	10.2	143	1	MILX_MOUSE
30	332.5	10.2	143	1	MILX_MOUSE
31	332.5	10.2	143	1	MILX_MOUSE
32	331.5	10.2	143	1	MILX_MOUSE
33	331	10.2	143	1	MILX_MOUSE

44	428	10.1	407	1	MILX_MOUSE
35	425	10.0	407	1	MILX_MOUSE
36	422.5	9.9	485	1	MILX_MOUSE
37	421.5	9.9	485	1	MILX_MOUSE
38	420.5	9.8	485	1	MILX_MOUSE
39	419.5	9.8	485	1	MILX_MOUSE
40	419	9.8	485	1	MILX_MOUSE
41	417	9.8	485	1	MILX_MOUSE
42	414	9.6	485	1	MILX_MOUSE
43	414	9.6	485	1	MILX_MOUSE
44	413.5	9.6	485	1	MILX_MOUSE
45	411	9.6	485	1	MILX_MOUSE

ALIGNMENTS

RESULT 1					
MILX_HUMAN		STANDARD	INT	613 AA	
ID	MILX_HUMAN				
AP	Q14985				
01	01 NOV 1997 (Ref. 35, created)				
02	01 NOV 1997 (Ref. 35, last sequence update)				
03	30 MAY 2000 (Ref. 39, last annotation update)				
04	Melanin related receptor (19)				
05	gpr50				
06	Human Sapiens (human)				
07	Farkas et al. Molecular Cloning of Human Melanin Receptor (hmelr) from Human Pituitary Gland				
08	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo				
09	NCBI Taxid 9606				
10	11				
11	SEQUENCE FROM N.A.				
12	TISSUE: pituitary				
13	RECORD: 9622896, EMBL 4 9647296				
14	Report S.M. Mayer D.R. Episawa T. Mable C.D.				
15	Ref. J. Biol. Chem. 271: 11717-11721 (1996)				
16	Cloning of a melanin-related receptor from human pituitary				
17	FEBS Lett. 386: 219-224 (1996)				
18	FUNCTION: DOES NOT BIND MELANIN				
19	CELLULAR LOCATION: Integral membrane protein				
20	TISSUE SPECIFICITY: HYPOTHALAMUS AND PITUITARY				
21	STIMULATIVE: BELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS				
22	This SwissProt entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Update by and for commercial and other purposes is allowed. (see http://www.ebi.ac.uk/submit/submit.html)				
23	or send an email to: license@ebi.ac.uk				
24	EMBL: 9622896, AF50614.1				
25	Gene: hmelr				
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00 Fukuyama: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 01 Articulata: Aves: Neognathae: Galliformes: Phasianidae: Phasianinae:
 02 Gallus:
 03 NEBL (accession).
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INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 466 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-466-104A-4

Query Match: 26,796 Score 869.51 DB 2: Length 466
 Best local similarity: 50.2%, Prod. No. 3,56,541
 Matches: 1531 Conserved: 721 Mismatches: 711 Indels: 97 Gaps: 7

DB 19 POPPEYPAALIFEMFANVITIVVDFNSAVTAVFENKRLNSGTFVSLVAADLVA 78
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 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1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 26

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CLASSIFICATION: 445
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/731,857
FILING DATE: 07-06-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, James K.
REGISTRATION NUMBER: 44,819
REFERENCE TO OTHER PATENTS:
PUBLICATION INFORMATION:
TELEPHONE: 617/542-5070
FAX: 617/542-8966
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
COMPOUND: lipid
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
OR 466-103A-15

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Query Match 26.28 Score 854.57 DB 2: Fourth 462
Best Local Similarity 19.78 Prod. No. 436-53
Matches 151 Conservative 767 Mismatches 461 Indels 11 Gaps 4

UY 17 KIDNEY TUBULE EPITHELIAL CELL TRANSFORMATION ASSAY 75
DB 42 KIDNEY TRANSFORMATION ASSAY 87
UY 76 TRANSFORMATION ASSAY 135
DB 88 TRANSFORMATION ASSAY 147
UY 136 TRANSFORMATION ASSAY 195
DB 148 TRANSFORMATION ASSAY 207
UY 196 TRANSFORMATION ASSAY 251
DB 208 TRANSFORMATION ASSAY 265
UY 252 TRANSFORMATION ASSAY 311
DB 256 TRANSFORMATION ASSAY 325
UY 312 TRANSFORMATION ASSAY 325
DB 426 TRANSFORMATION ASSAY 429

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RESULT: 11
US-08-466-103A-6
Sequence 6, Application US/08466103A
Patent No. 584124
GENERAL INFORMATION:
APPLICANT: Robert, Steven M.
APPLICANT: Robert, Steven M.
TITLE OF INVENTION: HIGH ACTIVITY RECEPTOR
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 29
ADDRESS: 1180 S. Richardson Blvd.
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 02110-2804
COMPOUND RELEVANCE: 100%
MOLECULE TYPE: DISKETTE
COMPOUND: IBM compatible

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OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/731,857
FILING DATE: 07-06-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, James K.
REGISTRATION NUMBER: 44,819
REFERENCE TO OTHER PATENTS:
PUBLICATION INFORMATION:
TELEPHONE: 617/542-5070
FAX: 617/542-8966
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
COMPOUND: lipid
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-466-103A-6

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Query Match 22.78 Score 740.57 DB 2: Fourth 286
Best Local Similarity 19.78 Prod. No. 440-45
Matches 142 Conservative 617 Mismatches 721 Indels 31 Gaps 21

UY 63 TRANSFORMATION ASSAY 122
DB 1 GENE TRANSFORMATION ASSAY 60
UY 123 TRANSFORMATION ASSAY 182
DB 61 TRANSFORMATION ASSAY 119
UY 192 TRANSFORMATION ASSAY 240
DB 120 TRANSFORMATION ASSAY 179
UY 241 TRANSFORMATION ASSAY 300
DB 180 TRANSFORMATION ASSAY 249
UY 401 TRANSFORMATION ASSAY 428
DB 210 TRANSFORMATION ASSAY 267

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RESULT: 11
US-08-466-103A-6
Sequence 8, Application US/08896465
Patent No. 5949264
GENERAL INFORMATION:
APPLICANT: Robert, Steven M.
APPLICANT: Robert, Steven M.
TITLE OF INVENTION: HIGH ACTIVITY RECEPTOR
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 25
ADDRESS: 1180 S. Richardson Blvd.
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 02110-2804

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,365
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 69/22,180
FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE TO PRIOR APPLICATIONS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
CELL TYPE: Melanocyte
US-08-896-365-H

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Query Match 2134, Score 692, DB 2, Length 257,
Best Local Similarity 49.28, Freq. No. 7,96,423,
Matches 119, Conservative 56, Mismatches 62, Indels 6, Gaps 23

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QY 82 VYLMHMSIGWLSGCGQWVGLIGLSVVGSLFVHVAATNRYVYTHSYGTEIPS 141
DB 1 YHAIASIVNWSSTSPHJSDHSEHVSIVSVPHTTALINWVCTHCHPYRSLYS 60
QY 142 VNTTIVITVIMKVLAVLPMVIGTIEYRRTYGLFVNTVITVITVITVITVIT 201
DB 61 STNSLGYVFLIMLIVAVINLGVLTQYDPRYSCTFQSVASATIAVAVHETVM 129
QY 202 LVVGVYVWKEVLAARDPACQNPV - QIAVNRITLTVITVITVITVITVITVIT 257
DB 121 LVVTVVETVAVIVVWVWV - FLSNPTFLFPGVETVAVIVVIVVITVITVITVIT 178
QY 258 VIVAVSVKPKKIPRMKYLAVITAVRSCINAVITGALNHRIRKRYVITVAKRITV 317
DB 179 LVVAVSVKPKRITKMLVASTVAVRSCINAVITGALNHRIRKRYVITVAKRITV 248
QY 318 EF 419
DB 249 EF 240

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RESULT 12
US-08-896-365-H
Sequence 9, Application US/08896365
Patent No. 5939264
GENERAL INFORMATION:
APPLICANT: Ecolab, LLC, Inc.
APPLICANT: Ingotio Christopher K.
APPLICANT: Messer, Lori A.
APPLICANT: Tonn, John, Jr.
TITLE OF INVENTION: GENETICALLY ENGINEERED BACTERIAL STRAINS
CURRENT FILING DATE: 1997-02-22
PUBLICATION DATE: 1998-02-11
ADDRESS: 701 Grand Avenue, Suite 3200,

```

```

STREET: 701 Grand Avenue, Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: USA
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,365
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 69/22,180
FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE TO PRIOR APPLICATIONS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
CELL TYPE: Melanocyte
US-08-896-365-H

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Query Match 1218, Score 594, DB 2, Length 153,
Best Local Similarity 45.28, Freq. No. 4,86,213,
Matches 70, Conservative 39, Mismatches 40, Indels 6, Gaps 32

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QY 127 VYVYHSLVYFVSVVET - QYVITVITVITVITVITVITVITVITVITVIT 184
DB 1 VYVYHSLVYFVSVVET - QYVITVITVITVITVITVITVITVITVITVIT 184
QY 185 RVVIVITVITVITVITVITVITVITVITVITVITVITVITVITVITVITVITVIT 242
DB 59 SSATVIAVAVVETVITVITVITVITVITVITVITVITVITVITVITVITVITVIT 118
QY 243 ELVAVWVTVITVITVITVITVITVITVITVITVITVITVITVITVITVITVITVIT 277
DB 119 ELVAVWVTVITVITVITVITVITVITVITVITVITVITVITVITVITVITVITVIT 153

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RESULT 13
US-08-255-608-H
Sequence 2, Application US/09255608
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Genetec, Inc.
APPLICANT: Genetec, Inc.
APPLICANT: Genetec, Inc.
TITLE OF INVENTION: Genetically Engineered Mammalian Neutrophils
CURRENT FILING DATE: 1997-02-22
PUBLICATION DATE: 1998-02-11
ADDRESS: 701 Grand Avenue, Suite 3200,

```


